SEQUENCE LISTING

<1<110> IRD

<120> BACTERIAL STRAINS OF GENUS EXIGOBACTERIUM, CULTURE METHOD AND USES

<130> 1721-94

<140> 10/538,715

<141> 2006-06-14

<150> PCT/FR03/003665

<151> 2003-12-10

<150> FR 02 15 865

<151> 2002-12-13

<160> 1

<170> PatentIn version 3.1

<210> 1
<211> 1510
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exiguobacterium acetylium

<220>
<221> misc_feature
<222> (1117)..(1117)
<223> unknown

<400> 1
gcgtgcctaa tacatgcaag tcgagcgcag gaagccgtct gaacccttcg gggggacgac 60

ggtggaatga gcggcggacg ggtgagtaac acgtaaagaa cctgcccata ggtctgggat 120

aaccacgaga aatcggggct aataccggat gtgtcatcgg accgcatggt ccgctgatga 180

aaggcgctcc ggcgtcgccc atggatggct ttgcggtgca ttagctagtt ggtggggtaa 240

cggcccacca aggcgacgat gcatagccga cctgagaggg tgatcggcca cactgggact 300

gagacacggc ccagactcct acgggaggca gcagtaggga atcttccaca atggacgaaa 360

gtctgatgga gcaacgccgc gtgaacgatg aaggctttcg ggtcgtaaag ttctgttgta 420

agggaagaac aagtgccgca ggcaatggcg gcaccttgac ggtaccttgc gagaaagcca 480

cggctaacta cgtgccagca gccgcggtaa tacgtaggtg gcaagcgttg tccggaatta 540

ttgggcgtaa agcgcgcgca ggcggcctct taagtctgat gtgaaagccc ccggctcaac 600

cggggagggc cattggaaac tgggaggctt gagtatagga gagaagagtg gaattccacg 660

tgtagcggtg aaatgcgtag agatgtggag gaacaccagt ggcgaaggcg actctttggc 720

ctataactga cgctgaggct gcgaaagcgt ggggagcaaa caggattaga taccctggta 780

gtccacgccg taaacgatga gtgctaggtg ttggagggtt tccgcccttc agtgctgaag 840

ctaacgcatt aagcactccg cctggggagt acggtcgcaa ggctgaaact caaaggaatt 900

gacggggacc cgcacaagcg gtggagcatg tggtttaatt cgaagcaacg cgaagaacct 960

taccaactct tgacatcccc ctgaccggta cagagatgta ccttcccctt cgggggcagg 1020

ggtgacaggt ggtgcatggt tgtcgtcagc tcgtgtcgtg agatgttggg ttaagtcccg 1080

caacgagcgc aacccttgtc cttagttgcc agcattnagt tgggcactct agggagactg 1140

ccggtgacaa accggaggaa ggtggggatg acgtcaaatc atcatgcccc ttatgagttg 1200

ggctacacac gtgctacaat ggacggtaca aagggcagcg aagccgcgag gtggagccaa 1260

tcccagaaag ccgttctcag ttcggattgc aggctgcaac tcgcctgcat gaagtcggaa 1320

tcgctagtaa tcgcaggtca gcatactgcg gtgaatacgt tcccgggtct tgtacacacc 1380

gcccgtcaca ccacgagagt ttgcaacacc cgaagtcggt gaggtaaccg taaggagcca 1440

gccgccgaag gtggggcaga tgattggggt gaagtcgtaa caaggtagcc gtatcggaag 1500

gtgcggctga 1510

cultures], 25 rue du Docteur Roux, 75015 Paris.

Advantageously, at least 70% of the genome of the strains of the invention is capable of hybridizing with the DNA of the deposited strain.

The invention is directed in particular toward the bacterial strains defined above, characterized by the sequence SEQ ID No. 1 of the 16S rRNA:

GCGTGCCTAATACATGCAAGTCGAGCGCAGGAAGCCGTCTGAACCCTTCGGGGGGACGACGGTGGAATGA
GCGGCGGACG
GGTGAGTAACACGTAAAGAACCTGCCCATAGGTCTGGGATAACCACGAGAAATCGGGGCTAATACCGGAT
GTGTCATCGG
ACCGCATGGTCCGCTGATGAAAGGCGCTCCGGCGTCGCCCATGGATGGCTTTGCGGTGCATTAGCTAGTT
GGTGGGGTAA
CGGCCCACCAAGGCGACGATGCATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGC
CCAGACTCCT
ACGGGAGGCAGCAGTAGGGAATCTTCCACAATGGACGAAAGTCTGATGGAGCAACGCCGCGTGAACGATG
AAGGCTTTCG
GGTCGTAAAGTTCTGTTGTAAGGGAAGAACAAGTGCCGCAGGCAATGGCGGCACCTTGACGGTACCTTGC
GAGAAAGCCA
CGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAA
AGCGCGCGCA
GGCGGCCTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGCCATTGGAAACTGGGAGGCTT
GAGTATAGGA
GAGAAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCG
ACTCTTTGGC
CTATAACTGACGCTGAGGCTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCG
TAAACGATGA
GTGCTAGGTGTTGGAGGGTTTCCGCCCTTCAGTGCTGAAGCTAACGCATTAAGCACTCCGCCTGGGGAGT
ACGGTCGCAA
GGCTGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACG
CGAAGAACCT
TACCAACTCTTGACATCCCCCTGACCGGTACAGAGATGTACCTTCCCCTTCGGGGGCAGGGGTGACAGGT
GGTGCATGGT
TGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCTTAGTTGCC
AGCATTnAGT
TGGGCACTCTAGGGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCC
TTATGAGTTG
GGCTACACACGTGCTACAATGGACGGTACAAAGGGCAGCGAAGCCGCGAGGTGGAGCCAATCCCAGAAAG
CCGTTCTCAG
TTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGTCGGAATCGCTAGTAATCGCAGGTCAGCATACTGCG
GTGAATACGT
TCCCGGGTCTTGTACACACCGCCCGTCACACCACGAGAGTTTGCAACACCCGAAGTCGGTGAGGTAACCG
TAAGGAGCCA
GCCGCCGAAGGTGGGGCAGATGATTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGA

or a sequence having more than 97% similarity with SEQ ID No. 1.

According to another aspect, these strains are characterized in that they are thermoresistant, saccharolytic and amylolytic and/or in that they are capable of producing lactate.